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Precautionary reference point estimates for northern Gulf of St. Lawrence (3Pn4RS) cod (*Gadus morhua*) and methods for their calculation

Estimation des points de référence pour l'approche de précaution pour la morue (*Gadus morhua*) du nord du golfe du Saint-Laurent (3Pn4RS) et méthodes pour leur calcul

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ABSTRACT

Six biomass limit reference points are estimated for northern Gulf of St. Lawrence (nGSL) cod. Five of these points are based on stock-recruit data while the sixth point is based purely on the concept of the minimum observed biomass from which there has been a recovery. In addition, two new methods for estimating reference points from stock-recruit data are introduced and estimated for nGSL cod. These new points should be evaluated on a variety of data sets, including simulated data and peer review before acceptance, though we introduce them here to place them in the context of other established methods. We conclude that for this stock, two of the six estimates can be considered credible for the stock using the 1974-2009 cohort reconstruction model output and place the biomass limit reference point at about 140,000 t spawning stock biomass (SSB) (this value was used in the 2009 assessment) We further suggest an upper stock reference point at about 200,000 t SSB which is a point above which there is little evidence of increased recruitment for an increase in SSB.

RÉSUMÉ

Six points de référence limites pour la biomasse de la morue du nord du golfe du Saint-Laurent (nGSL) ont été estimés. Cinq de ces points sont fondés sur des données stock-recrutement, tandis que le sixième n'est fondé que sur le concept de la biomasse minimale observée à partir de laquelle il y a eu rétablissement. En outre, deux nouvelles méthodes d'estimation des points de référence fondées sur des données stock-recrutement sont introduites pour la morue du nGSL. Ces nouveaux points devaient être évalués à l'aide d'un éventail d'ensembles de données, y compris des données de simulation, et faire l'objet d'un examen par des pairs avant d'être acceptés, mais nous les présentons ici afin de les comparer à d'autres méthodes établies. Notre conclusion est que, pour ce stock, deux des six estimations peuvent être considérés comme crédibles avec les résultats du modèle de reconstitution de la cohorte de 1974-2009 et qu'il faut fixer le point de référence limite de la biomasse à environ 140 000 t de biomasse du stock reproducteur (BSR) (valeur utilisée dans l'évaluation de 2009). Nous proposons en outre un niveau de référence supérieur pour ce stock d'environ 200 000 t de BSR, valeur au-delà de laquelle il existe peu de preuves d'accroissement du recrutement avec l'augmentation de la BSR.

INTRODUCTION

Precautionary reference points for the northern Gulf of St. Lawrence (nGSL) cod have not been estimated since 2003 (Zonal Assessment meeting held in Halifax in February, DFO 2003). Biomass limit reference points estimated at that meeting varied between 74,000 t and 275,000 t (DFO 2003) - Table 1, p. 38). Some of these methods were shown to be unreliable owing to problems in fitting particular stock- recruit curves, which discredited some of the higher estimates. Since 2003, it has been commonly suggested that the lowest Blim for this stock is in the 90,000 to 110,000 t range. Subsequently, various methods used to estimate these reference points were critically examined (DFO 2004) and several rejected. In particular the Serebryakov 50/90 method (Serebryakov 1991); (Serebryakov 1990) was rejected because of its tendency to produce lower Blim values as variance in the stock recruit plot increased, or when points became clustered near the origin (DFO 2004) p. 20). It was the Serebryakov method that produced the lowest estimate for Blim in 2003. Now with five more years of data, and the first zonal assessment for cod since 2003, as well as the fact that there have been many changes in nGSL cod VPA inputs since 2003, it is time to update our estimates of reference points for the stock and further develop the nGSL cod framework along the official accepted DFO precautionary approach (PA) framework (DFO 2006).

There has not been a strong incentive to re-estimate reference points for nGSL cod since 2003 because it has been accepted that nGSL cod SSB remains well below even the lowest of the estimates for Blim, for example, in 2008 SSB was estimated to be in the 26,000 t to 37,000 t range. Using even the lowest, and subsequently rejected, Blim value 74,000 t, this should compel management to focus on conservation and stock rebuilding. Clearly, this is still the case and it is unlikely that an increase in estimated value of Blim (as the Serebryakov 50/90 method has been rejected) will change the priority for conservation and stock growth. It is, however, increasingly common to make projections for this stock under various scenarios of fishing and productivity conditions and the biomass limit reference point estimates for the stock are used in the projections to determine the time when a growing exits the critical zone into the cautious zone (Duplisea and Hammill 2006); (Chassot *et al.* 2007); Yvan Lambert - IML, Mont-Joli, personal communication). Also, with this stock being listed as threatened by COSEWIC and a COSEWIC re-evaluation of the stock status occurring in 2009/10, the need for updated limit reference point estimates is warranted.

We present estimates of precautionary reference points for nGSL cod using some common and uncommon methods. We further provide a critical evaluation of the methods and the particular fittings in this case arriving at a set of points which we can consider to be justified reference point estimates for this stock at the present time given the available data.

METHODS

CANADIAN PA FRAMEWORK

DFO currently operates under a three zone model framework for development and implementation of the precautionary approach (DFO 2006) (Fig. 1). This framework consists of three zones: critical, cautious and healthy, which are divided by a biomass

limit reference point (Blim) and a biomass upper stock reference point (Busr). Blim is conceptually defined as the biomass below which the stock is considered to have suffered serious or irreversible harm. Busr is the biomass point above Blim which is general defined as some threshold in biomass below which the stock's productivity can be considered sub-optimal and thus action should be taken to bring the stock biomass above Busr. Busr has many characteristics of Bmsy though it is not necessarily Bmsy. It could for instance be a point where recruitment gains for an increase in stock size are very small.

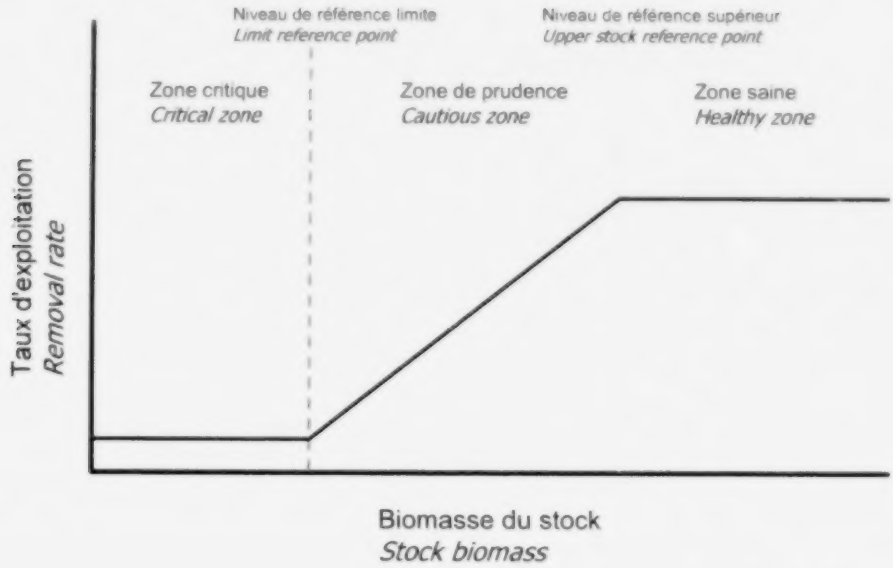

Figure 1: The framework for the precautionary approach used by the Canadian Department of Fisheries and Oceans (DFO 2006).

DATA

The data used here are from accepted ADAPT (Cohort reconstruction method - (Gavaris 1988) model run for nGSL cod from the Zonal Assessment meeting held in St John's in the winter of 2009 (DFO 2009). All the methods proposed here use spawning stock biomass (SSB) and recruitment at age 3 (R) series generated from ADAPT or in the case of the Bloss reference point (see below) only the SSB series (Annex 1). Weight at age used to calculate SSB was taken from the commericial fishery and as such is likely to create an upward bias in SSB and associated reference points.

The accepted ADAPT run for nGSL cod begins in 1974 and used the most recent reported data to arrive at a numbers at age vector for 1 January 2009, estimating natural mortality M in two blocks (DFO 2009). M was entered as 1974-1985, M=0.2; 1986-1996, M=0.4; and after 1996 M was estimated in blocks (Gregoire and Frechet 2005), 1997-2002, M=0.197; 2003-2008, M=0.284.

REFERENCE POINTS

Here we describe the methods and calculations of eight types of reference points (Table 1). These are roughly broken into three groups: "parametric" meaning that they are derived from fitting a parametric stock-recruit curve, "non-parametric" meaning that they are derived from non-parametric fitting methods, "empirical" meaning that they are based purely on some characteristic of the time series trend, e.g. lowest point. Furthermore, within the non-parametric group, two new reference points are explored based on the fitting of the non-parametric smoother curve fit to the stock-recruit data: Binfl and P0.1. A more detailed description of the reference points can be found below and are summarised in Table 1.

Table 1: A summary of reference points calculated here for 3Pn4RS cod. Binfl and P0.1 are new point introduced here and are discussed later in the document

NAME	DESCRIPTION	GROUP	POINT	EVALUATION	KEY REFERENCES
BH50	Beverton-Holt curve SSB @ 50% maximum recruitment	parametric	Blim	peer reviewed	(Myers *et al.* 1994)
HS50	Hockey stick curve SSB @ 50% maximum recruitment	parametric	Blim	peer reviewed	(Barrowman and Myers 2000); (O'Brien *et al.* 2003)
RK50	Ricker curve SSB @ 50% maximum recruitment	parametric	Blim	peer reviewed	(Myers *et al.* 1994)
NP50	Non-parameteric curve SSB @ 50% maximum recruitment	non-parametric	Blim	peer reviewed	(DFO 2004)
Binfl	Point of maximum change in R with a 1000 t change in SSB from smoother (NP50) curve	non-parametric	Potentially both Blim, Busr	not peer reviewed	
P0.1	SSB at 10% of cumulative smoother (NP50) recruitment predictions	non-parametric	Blim	not peer reviewed	
Sereb	Serebryakov 90% recruitment with 90% survival	non-parametric	Blim	peer reviewed	(Serebryakov 1991));(Myers *et al.* 1994); (DFO 2004)
Bloss	Lowest SSB from which there has been a recovery or 20% maximum SSB	empirical	Blim	peer reviewed	(ICES 2007)

BH50

The Beverton-Holt stock-recruit model is a two parameter model representing slope at the origin and asymptotic R. This can be fitted with common regression by linearising the model or using non-linear estimation. Here the model was fitted in R using the nls function. Once a fit to the data is obtained the reference point can be calculated as the SSB giving R equivalent to 50% of the asymptotic recruitment.

HS50

The hockey stick model draws a two line segmented regression, one segment being a flat line (slope 0) at a maximum recruitment and the other being a straight line from the origin meeting this flat segment. Finding the connection point between these two lines

(breakpoint) is not trivial and an iterative grid search method using Julious's algorithm is employed to do this (O'Brien *et al.* 2003). Once the segmented regression is fitted, the reference point calculation is trivial being the SSB giving R equivalent to 50% of the R in the flat section.

RK50

The Ricker stock-recruit model in an easily linearised two parameter model, having the characteristic of modelling density-dependent depressed R at high SSB. One of the parameters of the model describes the strength of this density dependence and thus affects the steepness of the so called "descending limb" of the Ricker curve. The reference point is similar to the other parametric curve which is the SSB giving the R equivalent to 50% of the maximum modelled R. Because of the descending limb with the Ricker curve, there can be two solutions for this problem, but the reference point is obviously the solution between 0 and SSB at maximum R.

NP50

Model-free interpolation of the SSB-R space is a highly desirable goal because it does not carry with it the mechanisms assumed in parametric SSB-R models. There are numerous such smoothing models such as splines, loess and local regressions, or even moving average models. Here, a cubic spline smoother was chosen. Cubic splines are relatively robust interpolators (Klasson 2008) commonly used in generalised additive models. Splines require an input parameter for the degree of smoother required in the form of degrees of freedom (df). Fortunately, objective methods exist for choosing reasonable df such as generalised cross validation (GCV), though a df choice by the user in not an unreasonable way to proceed provided the df considers data variability and the purpose for smoothing. Once a spline is fitted to the SSB-R data, then the reference point is chosen as the SSB giving the R equivalent to 50% of the maximum R predicted by the smoother. If multiple solutions are obtained, it is the smallest of the SSB values. This method does depend on there being some positive relationship between R and SSB but the smoother should not be so free as to create many maxima and minima.

Binfl

This reference point is based on the smoother fit in NP50. It is calculated by predicting R from the smoother over the observed SSB range for the stock in 1000 t increments. The difference between successive points is then calculated and the SSB at the place where the maximum difference occurs is the point of interest. It is not clear that this is either a limit reference point or even a larger points such as the upper stock reference (USR) (DFO 2006), though it is clear that a point of this nature should hold scientific and management interest because it is a reflection of where a stock will experience the greatest return in R for a unit increase in SSB (and the opposite). It may be that this point, in most cases, would be the USR but if there is a very steep slope at the origin from the smoother this point is likely to be quite low and perhaps too low for an USR thus more appropriately a Blim.

For stocks with low biomass, it should be done in smaller increments such that one should be aiming for hundreds of points for prediction. A uniqueness measure is provided for Binfl. Uniqueness is a measure of how unique the largest R change is for a unit change in SSB relative to all other R changes, it limits are 0 and 1. Uniqueness is calculated by determining the proportion of all R differences which are ≥80% of the maximum R change. Ideally, one would seek a more unique (i.e. uniqueness value

closer to 0) R difference which provides a more objective means of suggesting that one should not allow SSB to fall below the point because the R change there is uniquely large at that point.

Binfl is a reference point proposed here for the first time and has not received peer review or testing; therefore, it must be considered speculative presently.

P0.1

The non-parametric smoother curve can be used again to derive a reference point based on a definition of poor recruitment. Poor in this case is considered to be the 10th percentile of cumulated R. Like with Binfl, one constructs an SSB series over the observed SSB range but with regular increments, e.g. 1000 t. One then predicts R from the smoother for the SSB series and cumulates predicted R from the smallest to largest SSB in the time series. If one then takes the 10% of the cumulative R as a definition of poor R, one can determine the SSB where that occurs and this is the reference point. Clearly P0.1 would be a limit reference point because it is linked directly to poor R which would fit the definition of series harm. Alternatively, if one would like other kinds of reference points linked to other R levels like median or excellent recruitment they might choose other percentiles of cumulative R, e.g. 50%, 90%, respectively.

P0.1 is a reference point proposed here for the first time and has not received peer review or testing; therefore, it must be considered speculative presently.

Sereb

The Serebryakov reference points are related to the concept of stocks producing different percentiles of R under various survival conditions. The SB5090, is SSB at intersection between the median recruitment (50%) line and the 90% survival line. SB5090 then dictates that we are seeking an SSB where the stock under conditions of excellent survival should produce at least median recruitment. The SB9090 point used here dictates that one should have excellent recruitment when survival is excellent. One could use quantile regression to make this sort of calculation or alternatively one can often visually determine a line going through the origin for which 10% of the empirical points are above it and 90% are below it. Because there are a finite number of points, say 30 (30 years of data) as an example, one would find a line with 3 points above it and 27 below it. There are many lines in that interval however and depending on how the SSB-R scatter looks this might give quite different SSB at the intersection with the R quantile. One could then choose the mid point or any other with justification. There are many problems with this method (discussed below).

Bloss

Biomass at lowest observed spawning stock from which there has been a recovery is a classic reference point which is justified on the basis of two concepts: (1) we know that the stock has previously recovered from that point and (2) we do not know if the stock can recover from a lower biomass point. Inherently, therefore, Bloss should be strongly risk averse to phenomena like depensation (Myers *et al.* 1995) providing the productivity conditions for the stock have remained relatively stationary. Bloss, is probably the most easily justified limit reference point method and it is also very easily explained to stakeholders. ICES sometimes considers Bloss to be Blim and in other cases Bpa (which is larger than Blim) (ICES 2007). Canada does not use Bpa as a reference point

and clearly Bloss cannot be considered the upper stock reference point (USR) so Bloss can be considered a candidate only for Blim in the DFO framework.

In our calculations we defined recovery as 30% of K though recovery to other levels such as 50% Bmax (Bmsy proxy) may be more appropriate or 80% Bmsy (i.e. 40% K) which has been accepted as a default in DFO's Sustainable Fisheries Framework (http://www.dfo-mpo.gc.ca/fm-gp/peches-fisheries/fish-ren-peche/sff-cpd/overview-cadre-eng.htm). In the case where this has not happened, 20% SSBmax was chosen as the point and the year of occurrence is reported as NA. Though we make the 20% SSBmax calculation we do not consider it a useful proxy for Bloss.

All reference point calculations were performed in R using associated libraries.

RESULTS AND DISCUSSION

Eight different reference points are shown here. Of these points, it would generally be considered that all but Binfl could be considered biomass limit reference points under the DFO PA framework (DFO 2006).

Neither of the Beverton-Holt fitted parameters was significant (Fig. 2). The data configuration is such that non-linear fitting method initial conditions can influence the fit and that sensitivity is cause to question the Beverton-Holt fit. Likewise the Ricker model fit is not good, though the intercept is significant. Binfl splits the two clouds of R-SSB points in the same manner that the steepest point in a logistic curve is between the plateau and 0. Binfl has a uniqueness of 0.14 which means that 14% of all R increments for a change in SSB of 1000 t are within 20% of the maximum R increment value. P0.1 seems to identify the position where recruitment decreases quickly with decrements of SSB in manner reminiscent of a depensation curve. The Serebryakov 90/90 point is clearly determined by just a few points such as 1980 and 2009 and any retrospective changes in the model fits may have a significant impact on its value. There is no Bloss value but the closest thing would be the SSB at the start of the series in 1974 which was about 200,000 t.

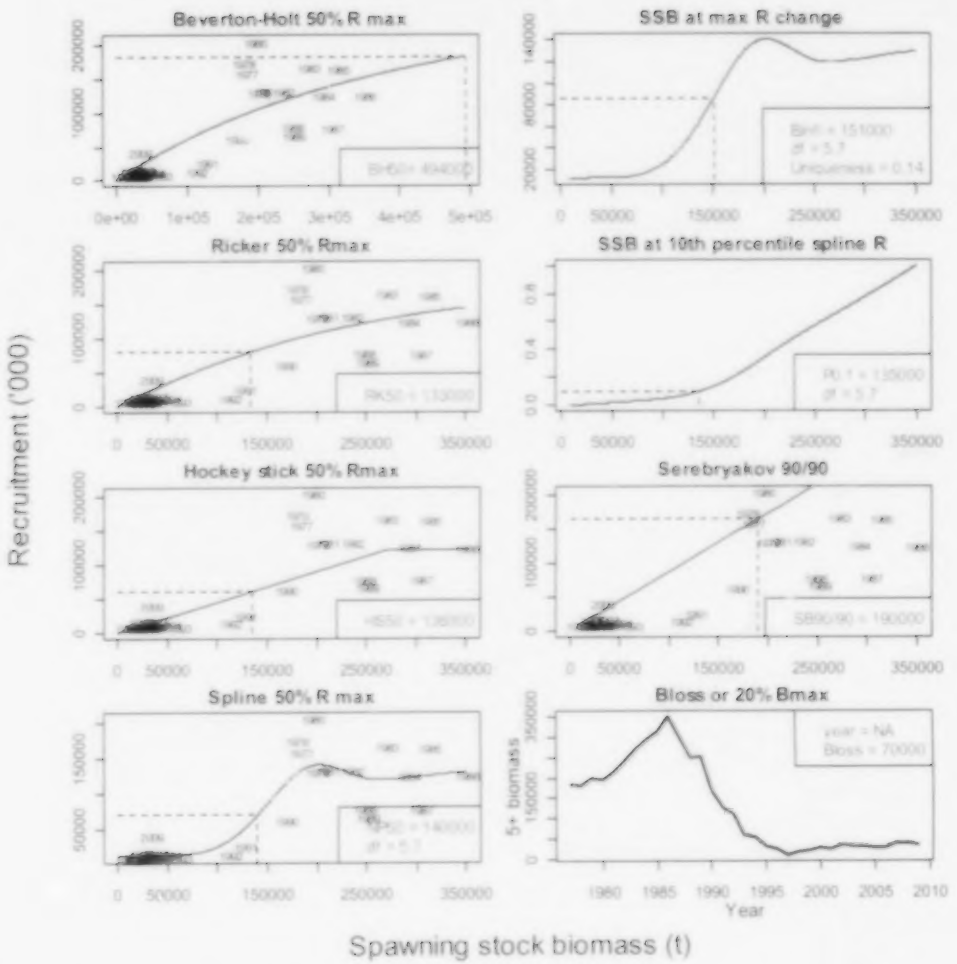

Figure 2: Spawner biomass precautionary reference point calculations for nGSL cod based on the accepted ADAPT run outputs from the 2009 zonal assessment meeting. For Bloss, when year=NA it means that there is no credible empirical Bloss and the value for Bloss shown = 20%Bmax.

Credibility of different reference points for 3Pn4RS cod in 2009

Each new fitting of reference points must be critically evaluated even when methods and points have previously been accepted. The reason for this is that most of these points depend on assessment model fitting and with the addition of new data, model fits can change and not always in terms of statistical improvement. For example it is becoming evident that when there is error in stock size estimates resulting from increased measurement error or increased variance in stock size, many stock-recruit based methods will underestimate the true limit reference point values (Cadigan 2009). For this reason, it would be wise to consider limit reference point estimates as liberal for stocks which have explored a large part of the R-SSB space. New data could reveal

characteristics of stock productivity never before observed and this could increase the uncertainty associated with model fits. Likewise, any change in productivity regime could invalidate reference points. This would not be symmetrical however. For example, if mean productivity for the period represented by the current estimates was relatively low, then an increased productivity situation would make the points more conservative and vice versa for a decrease in productivity. It is for these reasons, that is wise to regularly (but not too frequently) undertake a revaluation of the reference point framework. Consequently, the 6 years between the 2003 evaluation and the present is appropriate and very different reference point estimates have resulted.

BH50

The BH50 point cannot be considered credible for this stock. The problem with the model fitting is that its quality is low and it produces maximum recruitment at an SSB more than twice as large as the largest SSB ever observed in this stock, even the BH50 value itself is larger than the largest observed SSB for the stock. These characteristics of the model fit limit its utility presently.

HS50

The hockey model fit is considered to be one of the most credible functions describing stock-recruit data. Because of its simple assumptions and form (though complex to fit). We consider the HS50 fit to be a good estimate of Blim for this stock presently and it has been shown to be a good estimator for Canadian cod stocks (Shelton 2005).

RK50

The Ricker SSB-R curve fit is not considered credible for the current analysis as there is considerable variability in the 95% confidence interval of fitted coefficients. Nevertheless, the Ricker curve does not produce a descending limb, that is visible over the observed SSB range which the maximum R occurs near the maximum observed SSB, and the limit points from the method are very near other credible estimates. These characteristics suggest that the curve re-produces some feasible characteristics of stock production but the large variation in the model parameters means that we reject it. Because estimates are so near to those of other more credible methods, its inclusion or exclusion is unlikely to affect the overall estimate for the limit reference point.

NP50

The non-parametric spline smoother fit to the stock recruit data is a credible means of finding general relationship between R and SSB if there is monoticity at lower stock sizes. The smoother with a df parameter chosen by generalised cross validation has characteristics such as a maximum R level and a relatively linear increase to this level, thus it appears to be a parsimonious model of the R-SSB relationship. Its clear plateau easily allows the identification of a maximum R and thus 50% of this can be easily defined. The model smoothes over much of the noise in the R-SSB scatter which is desirable for reference point calculation. Presently, we consider the NP50 reference point to be highly credible.

Binfl and P0.1

These are interesting points that are experimental at present and have received no peer review. Though they may be useful reference point estimation methods we cannot

consider them credible until they have been tested on a variety of dataset, real and false, and peer reviewed. These points are discussed briefly below.

Sereb

Here, only the Serebryakov 90/90 point was calculated, though other points could be easily calculated. We chose the 90/90 point as it is more conservative than the 50/90 point which has been shown to have several problems such as being less conservative as scatter in the R-SSB space increases which is the opposite behaviour desired in a reference point (Shelton 2005). The 90/90 point will also suffer from these characteristics but its larger value makes it more reasonable. The 90/90 point is however not related to conditions of harm (that basis of a limit point) but is more target like because it relates to a desire for good recruitment under good survival. The 90th percentile survival line, however, is determined by only 3 point and it is difficult to justify a fitting based on so few points making the calculation strongly susceptible to type I error. We consider the Serebryakov point not to be credible presently.

Bloss

We have no true estimate of Bloss for this stock. The stock has never declined to a point where it has recovered (to a level 30% maximum SSB). In the present case therefore, a value of 20% SSB max was chosen, though this is arbitrary and we suggest that it is not a credible reference point as it is based purely on one large observation.

Interpreting two new reference points: Binfl and P0.1

The two new reference points derived from the non-parametric smoother through stock-recruit data hold a certain promise as reference points because they are well grounded in PA concepts such largest change in R for a unit change in SSB and points of poor recruitment.

Binfl, is based around many of the concepts explored by Rice and Mashal (Rice and Mashal 2003). Using sophisticated integration methods and an R which was considered "poor" these researchers determined the SSB at poor R. The present, uses the smoother as Rice and Mashal but selects the point where the smoother produces the larges change in R for a fixed change in SSB. For a smoother displaying strong compensatory dynamics (steep at the origin) this might be considered as a limit reference point. For a smoother displaying some depensatory like characteristics it may be able to determine a point near the depensation point as a limit. The point is likely to be quite risk averse to depensation because depensatory phenomena characteristically display small changes in R for large changes in SSB within a relatively large SSB range from the origin, i.e. within a certain range of the origin no change in SSB is likely to affect R. Likewise the point is unlikely to identify very large SSB points where R levels off. It is more likely that this point will split the SSB between two clouds of points in the R-SSB space shown the nGSL cod because the SSB-R curve has some logistic like characteristics. This method is therefore most likely to identify the middle of the cautious zone. Though the SSB in the middle of the cautious zone is not a reference point (DFO 2006), it may be useful in placing the other two reference points and also it could be used to help define when a harvest control rule may become more aggressive in dealing with fishing mortality.

P0.1 is a point based on the cumulative R that would be produced from a stock growing from the lowest to largest observed SSB and following the non-parametric curve productivity characteristics. If one takes a low quantile of this cumulative curve as being

a point of poor recruitment, then the SSB at that poor R quantile can be determined. This is clearly related to the concept of poor recruitment and would fit the criterion of "serious or irreversible harm". One could imagine that a stock with strong compensation would quickly start producing large R at small SSB and P0.1 would be relatively small as a result. Alternatively, if a stock displayed depensatory dynamics, it would not produce large R until SSB was also large and therefore P0.1 would also be large. These are the characteristics sought in a limit reference point though the method and the R quantile (definition of poor R) should be further explored.

RECOMMENDATION FOR REFERENCE POINTS FOR 3PN4RS COD

Given our credibility analysis of the reference points applied to 3Pn4RS cod, we consider two reference point estimates as credible values for Blim: HS50 and NP50. For the accepted ADAPT run from the 2009 zonal assessment meeting, these points are 136,000 t and 140,000, respectively. Thus a biomass limit reference point of about 140,000 t SSB seems justified by these analyses.

Table 2: Spawner biomass reference point estimates for nGSL (3Pn4RS) cod. Credibility is a binary switch (0=not credible or not tested, 1= credible) based on strengths and weaknesses outlined in section 3.1. Weight at age used for SSB calculation was from the commercial fishery.

Name	SSB Based on accepted 2009 ADAPT run	credibility
BH50	494000	0
HS50	136000	1
RK50	133000	0
NP50	140000	1
Binfl	151000	0
P0.1	135000	0
Sereb	169000	0
Bloss	NA	0

We note, once again (DFO 2003), that in the interval 100,000 – 200,000 t SSB there are few observations. We therefore consider it to be speculative to suggest such a precise estimate for the reference point. Given that current fisheries are estimated to be removing biomass of the stock at the equivalent of about its surplus production, it seems unlikely that the stock will grow to an SSB in this range for many years without a significant change in the management priorities for the stock. We are therefore unlikely to know more about the characteristics of the stock productivity in this relatively

unexplored SSB range for a long time and a more accurate estimate of Blim will probably not be forthcoming.

SSB calculation for Northern Gulf cod has traditionally been done using weight at age from the commercial fishery. Because commercial fisheries tend to select the fastest growing fish in the harvested age classes, use of this weight at age vector applied to the general population will tend to overestimate SSB and reference points. SPAs track individuals and not biomass, however, so this does not result in a bias in population size estimates but it can change the perception of the stock size which is most often cited in terms of SSB. Likewise, reference points will change with a change in the weight at age vector but their changes will still be consistent with the SSB series. Any future changes in weight at age for SSB calculation may thus change the perception of the stock size and productivity but consistent use of weight at age vectors will simply scale values and this will not affect advice consistent with a precautionary approach.

One of the main purposes of re-estimating reference points for this stock in 2009 is that projection simulation studies are being increasingly used as a tool to explore management options for the stock. We therefore have suggested that using these deceptively precise Blim estimate for the stock of 140,000 t SSB is entirely appropriate in the context of exploring management scenarios. We also suggest, however, that researchers must be careful not to equate recovery of a stock to Blim as true recovery of a stock should be to a healthy level and not just the threshold of serious harm. An upper stock reference point should be used as minimum recovery point. We suggest that a useful proxy for an upper stock reference point could be the SSB at the upper cloud of R-SSB points which is above equivalent to the SSB at the beginning of the flat part of the hockey stick curve and the non-parametric smoother curve which is about 200,000 t SSB.

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Annex 1: Stock-recruitment data

The stock-recruit data set from the February 2009 ADAPT run (DFO 2009) are presented here lagged by three years to account for recruitment at age 3 (thus the year represents the year of birth for the recruits reported while the SSB reported occurred three years earlier). Weight at age used for SSB calculation was from the commercial fishery.

YEAR-CLASS YEAR	R (10^3)	SSB (TONNES)
1977	159677	184 547
1978	175085	178 998
1979	131754	199 864
1980	205995	196 141
1981	133573	211 370
1982	133323	236 421
1983	168074	271 249
1984	126197	292 885
1985	165636	314 382
1986	125730	350 958
1987	78243	304 485
1988	79855	247 962
1989	67373	251 499
1990	63012	169 557
1991	27600	127 062
1992	15273	112 756
1993	10316	61 835
1994	14665	51 236
1995	9501	32 437
1996	17155	23 357
1997	9382	7 911
1998	9008	17 798
1999	9477	19 170
2000	8687	25 992
2001	12378	22 933
2002	10775	35 119
2003	9659	31 167
2004	10953	31 278
2005	10504	28 109
2006	11500	26 011
2007	17520	37 618
2008	12219	39 501
2009	42488	33 577

Annex 2: Reference point calculation functions in R

```
# Reference point functions written by Daniel Duplisea, Fisheries and Oceans
# Canada, Institut Maurice-Lamontagne, Mont-Joli, QC Canada G5H 3Z4.
# daniel.duplisea@dfo-mpo.gc.ca; tel 1 418 775 0881
# Use and distribute as you wish and at your own risk.
# March 2009.

# Julious grid search algorithms for the Hockey stick stock-recruit model
# were written by researchers at IEO, Spain.

# data.set needs to a be dataframe with appropriately lagged SSB-R
# data in columns containing at least the exactly named columns:
# "year","SSB","R" (case sensitive). You decide if you want the year
# to represent the year-class year or SSB year. Note that this choice
# will affect the year designation for Bloss.


################################################################################
################################################################################
# 50% maximum value from a fitted Beverton-Holt relationship
################################################################################
BH50.nls.f= function(data.set,max.recruitment=0){
  # Beverton Holt SSB@50% max R: BH50
  # using form R=a*S/(b+S), therefore b = BH50
  x= data.set
  # if maximum recruitment !=0 then that value is used and not fitted
  if (max.recruitment==0){
        # use nonlinear regregression to estimate BH curve
        nonlin.fit= nls(x$R ~ (BHa*x$SSB)/(BHb+x$SSB), data=x, start =
        list(BHa=max(x$R), BHb=1e5))
        BHa= coef(nonlin.fit)[1]
        BHb= coef(nonlin.fit)[2]
     }
  else if (max.recruitment!=0){
        BHa= max.recruitment
        x$SSB2= x$SSB*BHa
        # use nonlinear regregression to estimate BH curve
        nonlin.fit= nls(log(x$R) ~ log(x$SSB2/(BHb+x$SSB)), data=x, start =
        list(BHb=1000))
        BHb= coef(nonlin.fit)[1]
  }
  BH.fit<<- nonlin.fit
  # max R and SSB at max R from fitted curve
  half.Rmax= BHa/2
  BH50<<- round(BHb)

  # calculate the curve and plot, superimpose data
  SSB.series= seq(0,max(BH50,max(x$SSB)),by=1000)
  BH.curve= (BHa*SSB.series)/(BHb+SSB.series)
  plot(x$SSB,x$R,xlim=c(0,max(BH50,max(x$SSB))),ylim=c(0,max(x$R)),xlab=
    "SSB tonnes",ylab="Recruits '000", main="Beverton-Holt 50% R max",type="n")
  text(x$SSB,x$R,x$year,cex=.7)
  lines(SSB.series,BH.curve)
  #conf.ints= confint(BH.fit)
  #lines(SSB.series, (conf.ints[1,1]*SSB.series) / (conf.ints[2,1]+SSB.series),
   #   col="red",lty=4)
   #lines(SSB.series, (conf.ints[1,2]*SSB.series) / (conf.ints[2,2]+SSB.series),
   #   col="red",lty=4)

  # put some lines showing where the BH50 is and its value
  lines(c(0,BH50),c(half.Rmax,half.Rmax),lty=2)
  lines(c(BH50,BH50),c(0,half.Rmax),lty=2)
  legend("bottomright",legend=paste("BH50=",round(BH50/1000)*1000),text.col=
      "blue")
}
```

```
#############################################################################
#############################################################################
# RK50 biomass at 50% max recruitment from fitted ricker
#############################################################################
RK50.f= function(data.set){
  x= data.set
  resolution= 1000
        Ricker.lm<<- lm(log(x$R/x$SSB)~x$SSB)
        Ra.start= exp(Ricker.lm$coefficients[1])
        Rb.start= -Ricker.lm$coefficients[2]
        Rick.fit= nls(R~Ra*SSB*exp(-Rb*SSB),data=x,
                start=list(Ra=Ra.start,Rb=Rb.start))
                Ricker.nls<<- Rick.fit
        Ra=coef(Rick.fit)[1]
        Rb=coef(Rick.fit)[2]
        SSB.series= seq(0,max(x$SSB),by=1000)
        RK.curve= Ra*SSB.series*exp(-Rb*SSB.series)
        SSB.min.series= seq(0,2000000,by=resolution)
        R.min.series= Ra*SSB.min.series*exp(-Rb*SSB.min.series)
  plot(x$SSB,x$R,xlim=c(0,max(x$SSB)),ylim=c(0,max(x$R)),xlab="SSB tonnes",ylab=
      "Recruits '000",main="Ricker 50% Rmax",type="n")
  text(x$SSB,x$R,x$year,cex=.7)
  lines(SSB.series,RK.curve)
  #conf.ints= confint(Rick.fit)
  #lines(SSB.series,conf.ints[1,1]*SSB.series*exp(-conf.ints[2,1]*SSB.series),
  #    col="red",lty=4)
  #lines(SSB.series,conf.ints[1,2]*SSB.series*exp(-conf.ints[2,2]*SSB.series),
  #    col="red",lty=4)
  #Estimated RK50 from an easy method
  Rmax=max(R.min.series)
  position.Rmax= match(Rmax,R.min.series)
  half.Rmax= Rmax/2
  diffs= half.Rmax-R.min.series[0:position.Rmax]
  position.RK50 = match(min(abs(diffs)),abs(diffs))
  RK50 <<- SSB.min.series[position.RK50]
  # put some cosmetic lines showing where the RK50 is and its value
  lines(c(0,RK50),c(half.Rmax,half.Rmax),lty=2)
  lines(c(RK50,RK50),c(0,half.Rmax),lty=2)
  legend ("bottomright",legend= paste("RK50 =",RK50),text.col ="blue")
}

#############################################################################
#############################################################################
# Hockey stick 50% of max R (breakpoint)
#############################################################################
HS50.f= function(data.set){
  #the grid search subfunctions for the hockey stick breakpoint
  source("HS subfunctions.r")
  x=data.set

  # Apply Julious method
  jul.mod <- slm2.sr(x$SSB, x$R)
  # run changepoint.sr again with the specifications from jul.mod
  jul.mod <- changepoint.sr(x$SSB, x$R, delta=jul.mod$delta, constrained=T)

  # Grid search model
  gs.mod <- slm.sr(x$SSB, x$R, grid=500)
  # rerun changepoint.sr with the gs.mod results
  gs.mod <- changepoint.sr(x$SSB, x$R, delta=gs.mod$delta, constrained=T)

  # Plots, observed data and fitted model with 50% R max reference point
  plot(x$SSB,x$R,xlim=c(0,max(x$SSB)),ylim=c(0,max(x$R)),xlab="SSB tonnes",ylab=
      "Recruits '000",main="Hockey stick 50% Rmax",type="n")
  text(x$SSB,x$R,x$year,cex=.7)
  lines(c(0,jul.mod$delta), c(0, jul.mod$beta1*jul.mod$delta), lty=1)
  lines(c(jul.mod$delta, max(x$SSB)), c(jul.mod$alpha2, jul.mod$alpha2), lty=1)
  #lines(c(jul.mod$delta,jul.mod$delta),c(0,jul.mod$alpha2), col=2, lty=2)
  HS50<<- jul.mod$alpha2/(2*jul.mod$beta1)
  lines(c(0,HS50),c(jul.mod$alpha2/2,jul.mod$alpha2/2),lty=2)
```

```
  lines(c(HS50,HS50),c(0,jul.mod$alpha2/2), lty=2)
  legend("bottomright",legend=paste("HS50 =", round(HS50/1000)*1000),text.col =
      "blue")
}

#############################################################################
#############################################################################
#NP50.Blim=intersection of smoother through SR and median R from spline smoother
#############################################################################
NP50.f= function(data.set,DF.kernel=0,prop.Rmax=0.5,Origin=F){
  library(locfit)
  x= data.set
  #choose to include the origin as a point in the fitting
  if (Origin)
        x= rbind(rep(0,ncol(x)),x)
  plot(x$SSB,x$R,xlim=c(0,max(x$SSB)),xlab="SSB tonnes",ylab="Recruitment '000",
        main="Spline 50% R max",type="n")
  text(x$SSB,x$R,x$year,cex=.7)

  # put in your own kernel (DF of fit), or if 0 allow the function to choose it
  if (DF.kernel!=0){
        spline.fit= smooth.spline(x$SSB,x$R,df=DF.kernel)
        text(max(x$SSB),max(x$R)/3,labels="DF chosen by user",col=4,cex=1)
        }
        else if (DF.kernel==0){
    gcv.df= locfit(x$R~ lp(x$SSB,deg=3))$dp[7]
    #! I am not sure it is correct to use the GCV df in the spline. DD
        spline.fit= smooth.spline(x$SSB,x$R,df=gcv.df)
        }
 #generate an SSB series and predict R from smoother
 SSB.spline.series= seq(0,max(x$SSB),by=1000)
 R.50= prop.Rmax*max(predict(spline.fit,SSB.spline.series)$y)
 lines(SSB.spline.series,predict(spline.fit,SSB.spline.series)$y,lwd=1)
 # determine the - + inflection around recruitment median
 smth=predict(spline.fit,SSB.spline.series)$y-R.50
 # set - point=0 then divide lag1 series by itself to find NA
 smth[smth<0]=0
 smth2= c(smth[-1]/smth[-length(smth)],-99)
 # the intersection between R median and smoother is at inf points
 R.lims= is.infinite(smth2)
 # determine B where the inflections occured these are Blim of course the min
 # value is the true Blim as the smoother may cross median more than once.
 Blims= SSB.spline.series[R.lims]
 NP50<<- min(Blims)
 lines(c(0,NP50),c(R.50,R.50),lty=2)
 lines(c(NP50,NP50),c(0,R.50),lty=2)
 legend ("bottomright",legend= c(paste("NP50 =",NP50),
     paste("df =",round(spline.fit$df,1))),text.col ="blue")

 # a second reference point derived from the smoother. Biomass at the point
 # where the difference between two successive R points is the greatest. This
 # is a cheap approximation for finding the inflection point via derivatives.
 # Note though that it will be very sensitive to a bumpy smoothed curve as well
 # as the interval width chosen for the test SSB series. In this case we look
 # at 1000 t increments
 Binfl.f=function(data.set,fit=spline.fit){
       x= data.set
       integ.seq= seq(min(as.numeric(x$SSB)),max(as.numeric(x$SSB)),by=1000)
       pred.R= predict(fit,integ.seq)
       R= pred.R$y
       rdiffs= diff(R)
       inflection.position= match(max(rdiffs),rdiffs)
       Rinfl<<- R[inflection.position]
       Binfl<<- integ.seq[inflection.position]
       plot(pred.R$x,R,type="n",main="SSB at max R change",
              xlab="SSB",ylab="Recruitment from smoother fit")
       lines(pred.R$x,R)
       lines(c(0,Binfl),c(Rinfl,Rinfl),lty=2)
       lines(c(Binfl,Binfl),c(0,Rinfl),lty=2)
```

```
      # the % of points falling within 20% of the maximum difference. i.e. this
      # is a measure of the uniqueness of this particular difference. One would
      # want the difference to be fairly unique (the more points like it the
      # more arbitrary it is to choose it as a reference points because one
      # could choose many points like it and they may be quite different in SSB)
    Runique= round(length(rdiffs[rdiffs>(max(rdiffs)*.8)])/length(rdiffs),2)
          legend ("bottomright",legend= c(paste("Binfl =",round(Binfl/1000)*1000),
            paste("df =",round(spline.fit$df,1)),paste("Uniqueness =",Runique)),
            text.col ="blue")
  }
  Binfl.f(data.set)

  # a third reference point derived from the smoother.
  # Biomass at 10th percentile of recruitment from cumulated smoother points.
  # i.e. the point when recruitment is really bad.
  BRpoor.f=function(data.set,fit=spline.fit,P=0.1){
        x= data.set
        integ.seq= seq(min(as.numeric(x$SSB)),max(as.numeric(x$SSB)),by=100)
        pred.R= predict(fit,integ.seq)
        R= pred.R[[2]]
        totalB.spline= sum(R)
        R= R/totalB.spline
        SSB.position= match(P,round(cumsum(R),2))
        Ppoor<<- pred.R[[1]][SSB.position]
        plot(pred.R[[1]],cumsum(R),type="n",main="SSB at 10th percentile spline R",
              xlab="SSB",ylab="cumlative recruitment from smoother fit")
        lines(pred.R[[1]],cumsum(R))
        lines(c(0,Ppoor),c(P,P),lty=2)
        lines(c(Ppoor,Ppoor),c(0,P),lty=2)
          legend ("bottomright",legend= c(paste("P0.1 =",round(Ppoor/1000)*1000),
        paste("df =",round(spline.fit$df,1))),text.col ="blue")
  }
  BRpoor.f(data.set)
}

##############################################################################
##############################################################################
# Serebryakov 90-90 reference point
##############################################################################
Sereb.f= function(data.set,R.quantile=0.9,surv.line=0.9){
  # Sebreyakov 90 90
  # SB90/90:
  # the level of SSB corresponding to the intersection of the 90th
  # percentile of the recruitment observations and the replacement
  # line for which 10% of the S-R points are above the line.

  x= data.set
  plot(x$SSB,x$R,xlim=c(0,max(x$SSB)),ylim=c(0,max(x$R)),
        xlab="SSB tonnes",ylab="Recruitment '000",
        main=paste("Serebryakov ",R.quantile*100,"/",surv.line*100,sep=""),type="n")
    text(x$SSB,x$R,x$year,cex=.7)

  #use quantile regression to fit the survival line
  library(quantreg)
  survival.rq= rq(x$R~x$SSB - 1, tau=surv.line)

  # reference point and lines on plot
  R.quant= quantile(x$R,R.quantile)
  Sereb<<- R.quant/coef(survival.rq)
  lines(x$SSB[order(x$SSB)],predict(survival.rq)[order(x$SSB)],lty=1)
  lines(c(0,Sereb),c(R.quant,R.quant),lty=2)
  lines(c(Sereb,Sereb),c(0,R.quant),lty=2)
  legend("bottomright",legend=paste("SB",R.quantile*100,"/",surv.line*100," = ",
      floor(Sereb/1000)*1000,sep=""),text.col ="blue")
}

##############################################################################
##############################################################################
# Bloss Biomass at lowest observed stock size from which there has been a
```

```
# recovery to at least 30% Bmax
################################################################################
Bloss_f= function(data.set, Brec.perc=0.3){
  x=data.set
  x$Bloss= rep(NA,length(x$SSB))
  min.pos= match(x$SSB,min(x$SSB))
  B.rec= max(x$SSB)* Brec.perc # recovery is defined as x% of max observed SSB

  for (i in 1:length(x$SSB)){
    if (max(x$SSB[i:length(x$SSB)])>=B.rec) x$Bloss[i]=1
    }
  Bloss= min(x$SSB*x$Bloss, na.rm=T)
    #if Bloss is larger than 30% K it sets the Blim as 20%K
  if (Bloss> B.rec) Bloss=max(x$SSB)*0.2
  Bloss<<-Bloss
  Bloss.year= x$year[match(Bloss,x$SSB)]
  plot(input.data$year,input.data$SSB,type="l",main="Bloss or 20% Bmax",
      xlab="Year",ylab="SSB (t)",lwd=2)
  lines(c(min(x$year),Bloss.year),c(Bloss,Bloss),lty=2)
  lines(c(Bloss.year,Bloss.year),c(0,Bloss),lty=2)
  legend("topright",legend= c(paste("year =",Bloss.year),
      paste("Bloss =",round(Bloss/1000)*1000)),text.col ="blue")
#  mtext("SSB",side=2,line=2,outer=F,cex=0.8)
  mtext("5+ biomass",side=2,line=2,outer=F,cex=0.8)
  mtext("Year",side=1,line=2,outer=F,cex=0.8)
}
```

Annex 3: Hockey stick model subfunctions provided by IEO

```
# These functions need to be in a text file in your R working directory
############## hockey stockgrid search subfunction
slm.sr <- function(x, y, grid=100, lev=0.8){
  call <- match.call()
  if(length(x) != length(y)) stop ("x and y must have the same length")
  n <- length(x)
  delta.grid <- exp(seq(min(log(x)), max(log(x)), length=(grid+2)))
  out <- vector("numeric", 9)
  for (i in 2:(grid+1)){
    delta <- delta.grid[i]
    m <- changepoint.sr(x=x, y=y, delta=delta, constrained=T)
    out <- c(out, as.vector(unlist(m)[1:9]))
 }
 out <- as.data.frame(matrix(out, byrow=T, ncol=9)[-1,])
 names(out) <- c("xt","xtt","alpha1","beta1","alpha2","beta2","ssq","delta",
    "const")
 loglik <- -n/2*log(out$ssq) # up to a constant
 lim <- max(loglik) - qchisq(lev, 1)/2
# conf int calculations taken from gridsearch2.fun,O'Brien and Maxwell.
 interval <- c(NA,NA)
 index <- range((1:grid)[loglik >= lim])
 if(loglik[1]<lim){
   i <- index[1]
   interval[1] <-  out$delta[i-1] + ((lim-loglik[i-1])* (out$delta[i]-
      out$delta[i-1])/(loglik[i]-loglik[i-1]))
 }
 if(loglik[grid]<lim){
   i <- index[2]+1
   interval[2] <-  out$delta[i-1] + ((lim-loglik[i-1])* (out$delta[i]-
      out$delta[i-1])/(loglik[i]-loglik[i-1]))
 }
 out <- out[match(max(loglik), loglik),]
 row.names(out) <- ""
 out
}

#*******************************************************************************
#Código para segmented regression. Ver el fichero notes.
#leire, 28/11/2002
#*******************************************************************************
#En particular para el caso de la relación stock reclutamiento:

changepoint.sr <- function(x, y, delta, constrained=T){
 n <- length(x)
 half <- (x <= delta)
 t <- length(x[half])
 if(constrained){
  xmat <- cbind(rep(1,n))
  ymat <- c(log(y[half]), log(y[!half]))
  m <- lm(ymat ~ xmat - 1, offset=c(log(x[half]), rep(log(delta), n-t)) )
  beta <- as.vector(coef(m))
  beta <- exp(beta)
  beta <- c(0, beta[1], beta[1]*delta, 0)
  ypred <- predict(m)
  res <- ymat - ypred #log scale
  ssq <- sum(residuals(m)^2) #log scale
 }
 else{
  xmat <- cbind(c(rep(1,t), rep(0,n-t)), c(rep(0,t), rep(1,n-t)))
  ymat <- c(log(y[half]), log(y[!half]))
  m <- lm(ymat ~ xmat -1, offset=c(log(x[half]), rep(0, n-t)))
  beta <- as.vector(coef(m))
  beta <- exp(beta)
  beta <- c(0, beta[1], beta[2], 0)
  ypred <- predict(m)
```

```
  res <- ymat - ypred
  ssq <- sum(residuals(m)^2)
  delta <- beta[3] / beta[2] # calcula el punto de corte!!
 }
 out <- list(xt=max(x[half]), xtt=min(x[!half]), alpha1=beta[1], beta1=beta[2],
    alpha2=beta[3], beta2=beta[4], ssq=ssq, delta=delta, const=constrained,
    pred=ypred, res=res)
 out
}

#mod <- changepoint.sr(data$SSB, data$R, delta=200000, constrained=T)
#*******************************************************************************
#Utilizando grid search
slm.sr <- function(x, y, grid=100){
# for a unique cutpoint delta!! and a unique independent variable (y ~ x)
# weights=1
#grid >1
  call <- match.call()
  if(length(x) != length(y)) error ("x and y must have the same length")
  n <- length(x)
  delta.grid <- seq(min(x), max(x), length=grid)
  out <- vector("numeric", 9)
  for (i in 2:(grid-1)){
    delta <- delta.grid[i]
    m <- changepoint.sr(x=x, y=y, delta=delta, constrained=T)
    out <- c(out, as.vector(unlist(m)[1:9]))
 }
 out <- as.data.frame(matrix(out, byrow=T, ncol=9)[-1,])
 names(out) <- c("xt","xtt","alpha1","beta1","alpha2","beta2","ssq","delta",
    "const")
 mi <- min(out$ssq)
 out <- out[match(mi, out$ssq),]
 out
}

#*******************************************************************************
#Utilizando el algoritmo de Julious.
slm2.sr <- function(x,y){
  n <- length(x)
  xu <- unique(sort(x))
  nu <- length(xu)
  if(! nu >= 4) warning("Segmentation not possible")
# Fitting segmented model
  seg.mod <- vector("numeric", 10)
  for (i in 2:(nu-2)){
    delta <- (xu[i]+xu[i+1])/2
    mod <- changepoint.sr(x,y,delta,F)
    if(mod$delta >= mod$xt & mod$delta <= mod$xtt)
      mod$const <- T
    seg.mod <- c(seg.mod, as.vector(unlist(mod)[1:9]), i)
  }
  seg.mod <- as.data.frame(matrix(seg.mod, byrow=T, ncol=10)[-1,])
  names(seg.mod) <- c("xt","xtt","alpha1","beta1","alpha2","beta2","ssq",
      "delta", "const","index")
  if(length(seg.mod$const[seg.mod$const > 0]) > 0){
    min.const <- seg.mod[match(min(seg.mod$ssq[seg.mod$const>0]), seg.mod$ssq),]
  }
  else{
    min.const <- as.data.frame(matrix(c(rep(NA,6), 1e+20, NA, 1, 0),ncol=10))
    names(min.const) <- c("xt","xtt","alpha1","beta1","alpha2","beta2","ssq",
        "delta", "const", "index")
  }
  if(length(seg.mod$const[seg.mod$const >= 0]) > 0){
     while (length(seg.mod$const[seg.mod$const==0]) > 0){
       min.unconst <- seg.mod[match(min(seg.mod$ssq[seg.mod$const==0]),
          seg.mod$ssq),]
       seg.mod <- seg.mod[- match(min.unconst$index, seg.mod$index),]
       seg.mod$const[match(min.unconst$index, seg.mod$index)] <- 1
       m1 <- changepoint.sr(x=x, y=y, delta=min.unconst$xt, constrained=T)
```

```
      m2 <- changepoint.sr(x=x, y=y, delta=min.unconst$xtt, constrained=T)
      if (m1$ssq<=m2$ssq){
        seg.mod <- rbind(seg.mod, c(unlist(m1)[1:9], 0))
      }
      else{
        seg.mod <- rbind(seg.mod, c(unlist(m2)[1:9], 0))
      }
      min.const <- seg.mod[match(min(seg.mod$ssq[seg.mod$const>0]),
         seg.mod$ssq),]
    }
  }
  else{
   min.unconst <- as.data.frame(matrix(c(rep(NA,6), 1e+20, NA, 1, 0),ncol=10))
   names(min.unconst) <- c("xt","xtt","alpha1","beta1","alpha2","beta2","ssq",
       "delta", "const", "index")
  }
min.const
}

#*****************************************************************************
#Por cuestiones de memoria no guardo los residuos ni valores predecidos del
# modelo al ejecutar
#slm.sr y slm2.sr.
#Luego si son necesarios para dibujarlos o asi, se pueden calcular los residuos
# y los valores predecidos volviendo a ejecutar la función changepoint.sr
# restringido a juntarse en el delta que nos dan las funciones slm.sr, slm2.sr
#*****************************************************************************
#Bootstrap de los parámetros y del F estadistico
boot.sr <- function(x, y, iter, alpha=0.05){
  n <- length(x)
  m1 <- lm(log(y)~1)
  m1.ssq <- sum(residuals(m1)^2)
  pred <- predict(m1) # en escala log
  m2 <- slm2.sr(x,y)
  m2 <- changepoint.sr(x,y,delta=m2$delta, constrained=T)
  res <- as.vector(unlist(m2)[(10+n):(9+2*n)]) # en escala log
  beta.obs <- c(m2$alpha1, m2$beta1, m2$alpha2, m2$beta2, m2$delta)
  f.obs <- (m1.ssq - m2$ssq)*(n-2)/m2$ssq
  f.all <- f.obs
  beta <- c(m2$alpha1, m2$beta1, m2$alpha2, m2$beta2, m2$delta)
  for (i in 1:iter){
    print(i)
    yboot <- pred + sample(res)
    yboot <- as.vector(exp(yboot))
    m1boot <- lm(log(yboot)~1)
    m1boot.ssq <- sum(residuals(m1boot)^2)
    m2boot <- slm2.sr(x,yboot)
    f.all <- c(f.all, (m1boot.ssq - m2boot$ssq)*(n-2)/m2boot$ssq)
    beta <- c(beta, m2boot$alpha1, m2boot$beta1, m2boot$alpha2, m2boot$beta2,
        m2boot$delta)
  }
  f.all[f.all<0] <- 0
  p <- (length(f.all[f.all > f.all[1]]) / (iter+1))
  out <- list(beta=matrix(beta, byrow=T, ncol=5), beta.obs=beta.obs,
      f.obs=f.obs, p.value=p, f.all=f.all)
  out
}
#*****************************************************************************
#Como el bootstrap es muy intenso, o tal vez estoy guardando demasiadas cosas,
# lo voy a ir ejecutando en grupos de 100!!
#*****************************************************************************
#Bootstrap de un sólo elemento (de uno de los parámetros o del F estadistico)
boot2.sr <- function(x, y, iter, alpha=0.05){
  n <- length(x)
  m1 <- lm(log(y)~1)
  m1.ssq <- sum(residuals(m1)^2)
  pred <- predict(m1) # en escala log
  m2 <- slm2.sr(x,y)
  m2 <- changepoint.sr(x,y,delta=m2$delta, constrained=T)
```

```
  res <- as.vector(unlist(m2)[(10+n):(9+2*n)]) # en escala log
  f.obs <- (m1.ssq - m2$ssq)*(n-2)/m2$ssq
  f.all <- f.obs
  for (i in 1:iter){
    print(i)
    yboot <- pred + sample(res)
    yboot <- as.vector(exp(yboot))
    m1boot <- lm(log(yboot)~1)
    m1boot.ssq <- sum(residuals(m1boot)^2)
    m2boot <- slm2.sr(x,yboot)
    f.all <- c(f.all, (m1boot.ssq - m2boot$ssq)*(n-2)/m2boot$ssq)
  }
  f.all[f.all<0] <- 0
  p <- (length(f.all[f.all > f.all[1]]) / (iter+1))
   out <- list(f.obs=f.obs, f.all=f.all, p.value=p.value)
   out
}
```

Annex 4: Script to run the reference point functions

```
# you need the file input.data
### set working directory and import data, set your own working directory
  setwd("D:/papers & projects/PA/models")

### call the different reference point functions and plot in a single panel
  par(mfcol=c(4,2),mar=c(2,2,2,2),omi=c(0.5,0.50,0.15,0.15))
    BH50.nls.f(input.data) #Beverton Holt
    RK50.f(input.data)  # Ricker
    HS50.f(input.data)  # Hockey stick
    NP50.f(input.data)  # Non-parametric (spline)
    Sereb.f(input.data,R.quantile=0.9,surv.line=0.9)  # Serebryakov
    Bloss.f(input.data) #Bloss

   # Margin text
  mtext("Recruitment ('000)",side=2,line=2,outer=T, cex=1.2)
  mtext("Spawning stock biomass (t)",side=1,line=2,outer=T, cex=1.2)
```